

GenCore version 5.1.6  
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OM nucleic - protein search, using frame\_plus\_n2p model

Run on: March 18, 2004, 02:03:25 ; Search time 139.5 Seconds  
(without alignments)  
12796.027 Million cell updates/sec

Title: US-09-719-272-1

Perfect score: 1138

Sequence: 1 gatccgactgaaggactcc.....atttgaataatcagattttc 3467

Scoring table:

OLIGO  
Xgapop 60.0 , Xgapext 60.0  
Ygapop 60.0 , Ygapext 60.0  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 1045404 seqs, 257433775 residues

Word size: 1

Total number of hits satisfying chosen parameters: 2003896

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Command line parameters:

-MODEL=frame+ n2p model -DBV=xlp  
-Q=/cgn2\_1/USPTO.spool.p/US09719272/runat\_09032004\_085231\_7520/app.query.fasta\_1.3655  
-DB=Published Applications AA -QFMT=fastan -SUFFIX=rapb -MINMATCH=0.1  
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=coligo  
-TRANS=human40.cdi -LIST=45 -LOCALIGN=200 -THR\_SCORE=quality -THR\_MIN=1  
-ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0  
-MAXLEN=200000000 -USER=US09719272 @CGN\_1\_1\_23 @runat\_09032004\_085231\_7520  
-NCPU=6 -ICPU=3 -NO\_MMAP -LARGQUERY -NEG\_SCORES=0 -WAIT -DSPBLOCK=100  
-LONGLOG -DEV\_TIMEOUT=120 -WAEN\_TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60  
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

Database : Published Applications AA:

- 1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep.\*
- 2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep.\*
- 3: /cgn2\_6/ptodata/1/pubpaa/US05\_NEW\_PUB.pep.\*
- 4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep.\*
- 5: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep.\*
- 6: /cgn2\_6/ptodata/1/pubpaa/PCTUS\_PUBCOMB.pep.\*
- 7: /cgn2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB.pep.\*
- 8: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep.\*
- 9: /cgn2\_6/ptodata/1/pubpaa/US09A\_PUBCOMB.pep.\*
- 10: /cgn2\_6/ptodata/1/pubpaa/US09B\_PUBCOMB.pep.\*
- 11: /cgn2\_6/ptodata/1/pubpaa/US09C\_PUBCOMB.pep.\*
- 12: /cgn2\_6/ptodata/1/pubpaa/US09\_NEW\_PUB.pep.\*
- 13: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep.\*
- 14: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep.\*
- 15: /cgn2\_6/ptodata/1/pubpaa/US10C\_PUBCOMB.pep.\*
- 16: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pep.\*
- 17: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep.\*
- 18: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Query Match | Length | ID | Description |
|------------|-------------|--------|----|-------------|
|            |             |        |    |             |

|    |     |      |      |    |                      |                                    |
|----|-----|------|------|----|----------------------|------------------------------------|
| 1  | 607 | 53.3 | 647  | 15 | US-10-291-265-722    | Sequence 722, App                  |
| 2  | 607 | 53.3 | 1907 | 15 | US-10-291-265-250    | Sequence 250, App                  |
| 3  | 442 | 38.6 | 442  | 9  | US-09-925-300-950    | Sequence 30, App                   |
| 4  | 296 | 26.0 | 296  | 14 | US-10-374-539-3      | Sequence 9, Appl                   |
| 5  | 296 | 26.0 | 296  | 15 | US-10-374-499-9      | Sequence 13, Appl                  |
| 6  | 289 | 25.4 | 289  | 14 | US-10-314-232-13     | Sequence 8, Appl                   |
| 7  | 202 | 17.8 | 306  | 9  | US-09-788-626-8      | Sequence 27, Appl                  |
| 8  | 197 | 17.3 | 294  | 9  | US-09-788-626-27     | Sequence 54, Appl                  |
| 9  | 59  | 5.2  | 1502 | 9  | US-09-808-602-54     | Sequence 44, Appl                  |
| 10 | 59  | 5.2  | 1502 | 10 | US-09-800-198-44     | Sequence 55, Appl                  |
| 11 | 59  | 5.2  | 1948 | 9  | US-09-808-602-55     | Sequence 45, Appl                  |
| 12 | 59  | 5.2  | 1948 | 10 | US-09-800-198-45     | Sequence 29636, A                  |
| 13 | 55  | 4.9  | 57   | 14 | US-10-029-386-29636  | Sequence 12, Appl                  |
| 14 | 40  | 3.5  | 1495 | 15 | US-10-258-666-12     | Sequence 38, Appl                  |
| 15 | 34  | 3.0  | 2029 | 12 | US-10-087-684-38     | Sequence 38, Appl                  |
| 16 | 34  | 3.0  | 2029 | 12 | US-10-218-779-38     | Sequence 39, Appl                  |
| 17 | 34  | 3.0  | 2037 | 12 | US-10-087-684-39     | Sequence 39, Appl                  |
| 18 | 34  | 3.0  | 2037 | 12 | US-10-218-779-39     | Sequence 191, App                  |
| 19 | 30  | 2.6  | 162  | 15 | US-10-334-143-191    | Sequence 30320, A                  |
| 20 | 29  | 2.5  | 64   | 14 | US-10-029-386-30320  | Sequence 21, Appl                  |
| 21 | 20  | 1.8  | 20   | 14 | US-10-340-288-21     | Sequence 28, Appl                  |
| 22 | 15  | 1.3  | 20   | 14 | US-10-340-288-28     | Sequence 9, Appl                   |
| 23 | 176 | 1.2  | 176  | 14 | US-10-314-232-9      | Sequence 11, Appl                  |
| 24 | 14  | 1.2  | 289  | 14 | US-10-314-232-47     | Sequence 47, Appl                  |
| 25 | 14  | 1.2  | 322  | 14 | US-10-314-232-11     | Sequence 6, Appl                   |
| 26 | 14  | 1.2  | 354  | 10 | US-09-095-478-6      | Sequence 8, Appl                   |
| 27 | 14  | 1.2  | 379  | 10 | US-09-095-478-8      | Sequence 15, Appl                  |
| 28 | 14  | 1.2  | 401  | 14 | US-10-314-232-15     | Sequence 1, Appl                   |
| 29 | 14  | 1.2  | 412  | 10 | US-09-095-478-3      | Sequence 2, Appl                   |
| 30 | 14  | 1.2  | 426  | 10 | US-09-095-478-1      | Sequence 22, Appl                  |
| 31 | 14  | 1.2  | 463  | 10 | US-09-095-478-2      | Sequence 6, Appl                   |
| 32 | 14  | 1.2  | 898  | 14 | US-10-314-232-22     | Sequence 2, Appl                   |
| 33 | 14  | 1.2  | 2281 | 12 | US-10-087-684-6      | Sequence 10, Appl                  |
| 34 | 14  | 1.2  | 2281 | 12 | US-10-218-779-6      | Sequence 4, Appl                   |
| 35 | 14  | 1.2  | 2291 | 10 | US-09-822-871-2      | Sequence 37, Appl                  |
| 36 | 14  | 1.2  | 2300 | 12 | US-10-087-684-10     | Sequence 25, Appl                  |
| 37 | 14  | 1.2  | 2300 | 12 | US-10-218-779-10     | Sequence 85, Appl                  |
| 38 | 14  | 1.2  | 2301 | 10 | US-09-822-871-4      | Sequence 158623, Sequence 323, App |
| 39 | 14  | 1.2  | 2302 | 12 | US-10-087-684-37     | Sequence 95, Appl                  |
| 40 | 14  | 1.2  | 2302 | 12 | US-10-218-779-37     |                                    |
| 41 | 12  | 1.1  | 20   | 14 | US-10-340-288-25     |                                    |
| 42 | 12  | 1.1  | 33   | 15 | US-10-052-648A-85    |                                    |
| 43 | 12  | 1.1  | 56   | 12 | US-10-424-599-158623 |                                    |
| 44 | 12  | 1.1  | 98   | 15 | US-10-074-978A-323   |                                    |
| 45 | 12  | 1.1  | 105  | 12 | US-10-087-684-95     |                                    |

ALIGNMENTS

RESULT 1  
US-10-291-265-722  
; Sequence 722, Application US/10291265  
; Publication No. US20030232054A1  
; GENERAL INFORMATION:  
; APPLICANT: Hvaeq. Inc.  
; APPLICANT: Tang et al  
; TITLE OF INVENTION: No. US20030232054A1el Nucleic Acids and Polypeptides  
; FILE REFERENCE: 21272-017 (785)  
; CURRENT APPLICATION NUMBER: US/10/291,265  
; CURRENT FILING DATE: 2000-01-25  
; PRIOR APPLICATION NUMBER: 09/491,404  
; PRIOR FILING DATE: 2000-01-25  
; PRIOR APPLICATION NUMBER: 09/617,746  
; PRIOR FILING DATE: 2000-07-17  
; PRIOR APPLICATION NUMBER: 09/631,451  
; PRIOR FILING DATE: 2000-08-03  
; PRIOR APPLICATION NUMBER: 09/633,870  
; PRIOR FILING DATE: 2000-09-15  
; NUMBER OF SEQ ID NOS: 944  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 722  
; LENGTH: 647  
; TYPE: PRT

ORGANISM: Homo sapiens  
US-10-291-265-722

Alignment Scores:  
Pred. No.: 0 Length: 647  
Score: 607.00 Matches: 607  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 53.34% Indels: 0  
DB: 15 Gaps: 0

US-09-719-272-1 (1-3467) x US-10-291-265-722 (1-647)

|    |     |  |     |
|----|-----|--|-----|
| QY | 6   | GGACTGAGGACTCTCTGCTGGCCCACTCTCTGACCCCTGTGGAGATGGGAGGCTCAAC   | 65  |
| DB | 41  | GlyLeuLeuAspSerLeuLeuAlaHisSerSerAspProValGluMetArgArgLeuAn  | 60  |
| QY | 66  | TACCAGACCCAGGTATGGAGACCAACCCACCCATCCCATCACCCAGCTGGCGGACAAC   | 125 |
| DB | 61  | TyrGlnThrProGlyMetArgAspHisProProIleProIleThrAspLeuAlaAspAn  | 80  |
| QY | 126 | ATCGAGCGCTCAAGCCCAAGTGGCTCAAGTTCTCCAGAGTATGAGTCCATCGAC       | 185 |
| DB | 81  | IleGluArgLeuLeuAlaAsnAspGlyLeuLeuPheSerGlnGluTyrGluSerIleAsp | 100 |
| QY | 186 | CCTGGACAGAGTTCAGTGGGAGATTCAAACCTGGAGGTGAACAAGCCCAAGACCGC     | 245 |
| DB | 101 | ProGlyGlnGlnPheThrTrpGluAsnSerAsnLeuGluValAsnLysProLysAsnArg | 120 |
| QY | 246 | TATGCGAATGTATCGCTACGACCACTCTCGAGTCACTCTACCTCTATCGATGGCGTC    | 305 |
| DB | 121 | TyrAlaAsnValIleAlaTyrAspHisSerArgValIleLeuThrSerIleAspGlyVal | 140 |
| QY | 306 | CCCGGAGTGACTACATCAATGCAATCATCATGATGGCTACCGCAAGCAGAAATGCTAC   | 365 |
| DB | 141 | ProGlySerAspTyrIleAsnAlaAsnTyrIleAspGlyTyrArgLysGlnAsnAlaTyr | 160 |
| QY | 366 | ATGCCACGAGGCGCCCTGCGGAGACCATGGCGATTTCTGGAGATGCTGGGAA         | 425 |
| DB | 161 | IleAlaThrGlnGlyProLeuProGluThrMetGlyAspPheTrpArgMetValTrpGlu | 180 |
| QY | 426 | CACGACGCGCCACTGTGGTCATGATGACACCGCTGGAGGAGAGTCCCGGTAAATGT     | 485 |
| DB | 181 | GlnArgThrAlaThrValValMetMetThrArgLeuGluGluLysSerArgValLysCys | 200 |
| QY | 486 | GATCAGTACTGGCCAGCCCGTGGACCGACACTGTGGCCCTTATTCAGGTGACCTGTG    | 545 |
| DB | 201 | AspGlnTyrTrpProAlaArgGlyThrGluThrCysGlyLeuIleGlnValThrLeuLeu | 220 |
| QY | 546 | GACACAGTGGAGTGGCCCATACACTGTGCGCACTTCGCACCTCCACAGAGTGGCTCC    | 605 |
| DB | 221 | AspThrValGluLeuAlaThrTyrThrValArgThrPheAlaLeuHisLysSerGlySer | 240 |
| QY | 606 | AGTGAGAAGCGTGCAGTGGCTCAGTTTCAGTTTCATGGCCCTGGCCAGACCATGAGTTCT | 665 |
| DB | 241 | SerGluLysArgGluLeuArgGlnPheGlnPheMetAlaTrpProAspHisGlyValPro | 260 |
| QY | 666 | GAGTACCCAACTCCCACTCCCTGCTTCTACAGCGGTCAAGCGCTGCAACCCCTAGAC    | 725 |
| DB | 261 | GluTyrProThrProIleLeuAlaPheLeuArgArgValLysAlaCysAsnProLeuAsp | 280 |
| QY | 726 | GCAGGGCCCATGTGTGTGCTACCTGCGCGGGCTGGCGCCACCGCTCTCATCGTG       | 785 |
| DB | 281 | AlaGlyProMetValValHisCysSerAlaGlyValGlyArgThrGlyCysPheIleVal | 300 |
| QY | 786 | ATTGATGCCATGTGGAGCGGATGAACAGCAGAGACGCTGACATCTATGGCCACGTG     | 845 |
| DB | 301 | IleAspAlaMetLeuGluArgMetLysHisGluLysThrValAspIleTyrGlyHisVal | 320 |
| QY | 846 | ACCTGATGCGATCAGAGGAACTCATGTGTGAGACGAGGACCAAGTACGTGTTCAATC    | 905 |
| DB | 321 | ThrCysMetArgSerGlnArgAsnTyrMetValGlnThrGluAspGlnTyrValPheIle | 340 |

|    |      |  |      |
|----|------|--|------|
| QY | 906  | CATGAGGCGCTGCTGAGGCTGCCAGCTGGCGCCACACAGAGGTGCTGCTCCCGCAACCTG | 965  |
| DB | 341  | HisGluAlaLeuLeuGluAlaAlaThrCysGlyHisThrGluValProAlaArgAnLeu  | 360  |
| QY | 966  | TATGCCACATCCAGAAGCTGGGCCAAGTGCCTCCAGGGAGAGTGTGACCCCATGGAG    | 1025 |
| DB | 361  | TyrAlaHisIleGlnLysLeuGlyGlnValProProGlyGluSerValThrAlaMetGlu | 380  |
| QY | 1026 | CTCGAGTTCAAGTGTCTGGCAGCTCCAGGCCCAAGCTCCCGCTTCATCAGCCCAAC     | 1085 |
| DB | 381  | LeuGluPheLysLeuLeuAlaSerSerLysAlaHisThrSerArgPheIleSerAlaAn  | 400  |
| QY | 1086 | CTGCCCTGCAACAAGTTCAGAAACCGCTGGTGAACATCATCCCTACGAATGGACCGT    | 1145 |
| DB | 401  | LeuProCysAsnLysPheLysAsnArgLeuValAsnIleMetProTyrGluLeuThrArg | 420  |
| QY | 1146 | GTGTGTCTGCACCCCATCGTGTGTGGAGGCTCTGACTACATCAATGCCAGTTCCTG     | 1205 |
| DB | 421  | ValCysLeuGlnProIleArgGlyValGluGlySerAspTyrIleAsnAlaSerPheLeu | 440  |
| QY | 1206 | GATGTTATAGACAGCAGAGGCCCTACATAGCTACACAGGGGCTCTGGCAGAGCACCC    | 1265 |
| DB | 441  | AspGlyTyrArgGlnGlnLysAlaTyrIleAlaThrGlnGlyProLeuAlaGluSerThr | 460  |
| QY | 1266 | GAGGACTTCTGGCGCATGCTATGGAGCACAATTCACCACATCATGCTATGCTGACCAAG  | 1325 |
| DB | 461  | GluAspPheTrpArgMetLeuTrpGluHisAsnSerThrIleValMetLeuThrLys    | 480  |
| QY | 1326 | CTTCGGAGATGGGAGGAGAAATGCCACCACTACTGGCCAGCAGAGCGCTCTGCTCGC    | 1385 |
| DB | 481  | LeuArgGluMetGlyArgGluLysCysHisGlnTyrTrpProAlaGluArgSerAlaArg | 500  |
| QY | 1386 | TACCACTACTTTGTGTGACCGGATGGCTGAGTACACATGCCAGTATATCTCGCT       | 1445 |
| DB | 501  | TyrGlnTyrPheValValAspProMetAlaGluTyrAsnMetProGlnTyrIleLeuArg | 520  |
| QY | 1446 | GAGTTCAAGCTCACGGATGCCGGATGGCAGTCAAGACCAATCCGGCAGTTCAGATTTC   | 1505 |
| DB | 521  | GluPheLysValThrAspAlaArgAspGlyGlnSerArgThrIleArgGlnPheGlnPhe | 540  |
| QY | 1506 | ACAGACTGCCAGAGCAGGCGCTGCCAAGACAGCGGAGGATTCATTGACTTCATCGGG    | 1565 |
| DB | 541  | ThrAspTrpProGluGlnGlyValProLysThrGlyGluGlyPheIleAspPheIleGly | 560  |
| QY | 1566 | CAGGTGCATAAGCAAGGAGCAGTTGGACAGGATGGSCCTATCACGTCGACATGCACT    | 1625 |
| DB | 561  | GlnValHisLysThrLysGlnPheGlyGlnAspGlyProIleThrValHisCysSer    | 580  |
| QY | 1626 | GCTGGCGTGGCGCCACCGGGTGTTCATCTCTGAGCATGCTCTCGAGCGCATCGCC      | 1685 |
| DB | 581  | AlaGlyValGlyArgThrGlyValPheIleThrLeuSerIleValLeuGluArgMetArg | 600  |
| QY | 1686 | TATGAGGCGTGGTCGACATGTTTCAGACCTGAGACCCCTCGGTACACAGCGTCTCGCC   | 1745 |
| DB | 601  | TyrGluGlyValValAspMetPheGlnThrValLysThrLeuArgThrGlnArgProAla | 620  |
| QY | 1746 | ATGCTGCACAGAGGACCATGATCAGCTGCTGCTACCGTGGCGCCCTGAGTACCTCGCC   | 1805 |
| DB | 621  | MetValGlnThrGluAspGlnTyrGlnLeuCysTyrArgAlaAlaLeuGluTyrLeuGly | 640  |
| QY | 1806 | AGCTTTGACCACTATGCAACG  | 1826 |
| DB | 641  | SerPheAspHisTyrAlaThr  | 647  |

RESULT 2

US-10-291-265-250  
; Sequence 250, Application US/10291265  
; Publication No. US20030232054A1  
; GENERAL INFORMATION:  
; APPLICANT: Hyseq, Inc.  
; APPLICANT: Tang et al  
; TITLE OF INVENTION: No. US20030232054A1 Nucleic Acids and Polypeptides  
; FILE REFERENCE: 21272-017 (785)

; CURRENT APPLICATION NUMBER: US/10/291,265  
 ; CURRENT FILING DATE: 2000-01-25  
 ; PRIOR APPLICATION NUMBER: 09/491,404  
 ; PRIOR FILING DATE: 2000-01-25  
 ; PRIOR APPLICATION NUMBER: 09/617,746  
 ; PRIOR FILING DATE: 2000-07-17  
 ; PRIOR APPLICATION NUMBER: 09/631,451  
 ; PRIOR FILING DATE: 2000-08-03  
 ; PRIOR APPLICATION NUMBER: 09/633,870  
 ; PRIOR FILING DATE: 2000-09-15  
 ; NUMBER OF SEQ ID NOS: 944  
 ; SOFTWARE: FastSeq for Windows Version 3.0  
 ; SEQ ID NO 250  
 ; LENGTH: 1907  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 ; US-10-291-265-250

Alignment Scores:  
 Pred. No.: 0 Length: 1907  
 Score: 607.00 Matches: 607  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 53.34% Indels: 0  
 DB: 15 Gaps: 0

US-09-719-272-1 (1-3467) x US-10-291-265-250 (1-1907)

|    |      |  |      |
|----|------|--|------|
| Qy | 6    | GGACTGAAGGACTCTTGTCTGGCCCACTCTCTGACCCCTGTGGAGATGCGGAGGCTCAAC | 65   |
| Db | 1301 | GlyLeuLysAspSerLeuLeuAlaHisSerSerAspProValGluMetArgArgLeuAsn | 1320 |
| Qy | 66   | TACGAGACCCAGGTATGCGAGACACACCCACCCATCCCATCACGACCTGGCGGCAAC    | 125  |
| Db | 1321 | TyrGlnThrProGlyMetArgAspHisProProileProileThrAspLeuAlaAspAsn | 1340 |
| Qy | 126  | ATCGAGCGCTCAAGCCCAAGCGGCTCAAGTTCTCCAGGAGTATGATGCTCATCGAC     | 185  |
| Db | 1341 | IleGluArgLeuLysAlaAsnAspGlyLeuLysPheSerGlnGlyThrGlySerIleAsp | 1360 |
| Qy | 186  | CCTGGACAGCAGTTCACGTGGGAGATTCAAACTGGAGGTGAACAAGCCCAAGACCGC    | 245  |
| Db | 1361 | ProGlyGlnPheThrTrpGluAsnSerAsnLeuGluValAsnLysProLysAsnArg    | 1380 |
| Qy | 246  | TATCGGAATGTCATCGCTAGACACATCTCGAGTCACTCTTACTCTATCGATGGGTC     | 305  |
| Db | 1381 | TyrAlaAsnValIleAlaTyrAspHisSerArgValIleLeuThrSerIleAspGlyVal | 1400 |
| Qy | 306  | CCGGGAGTGACTACATCAATGCCAACTACATCGATGGCTACCGCAAGCAGATGCTTAC   | 365  |
| Db | 1401 | ProGlySerAspTyrIleAsnAlaAsnTyrIleAspGlyTyrArgLysGlnAsnAlaTyr | 1420 |
| Qy | 366  | ATCGCCACGAGGCCCCCTGCTCCGAGACCATGGCGGATTTCTGGAGAATGGTGGGAA    | 425  |
| Db | 1421 | IleAlaThrGlnGlyProLeuProGluThrMetGlyAspPheTrpArgMetValTrpGlu | 1440 |
| Qy | 426  | CAGCGCAGCGGCACTGTGTGATGATGACAGCGCTGGAGGAGAGTCCCGGGTAAATGT    | 485  |
| Db | 1441 | GlnArgThrAlaThrValValMetMetThrArgLeuGluLysSerArgValLysCys    | 1460 |
| Qy | 486  | GATCAGTACTGGCGCCGCGGACCGAGACCTGTGGCCCTTATTCAGGTGACCTGTG      | 545  |
| Db | 1461 | AspGlnTyrTrpProAlaArgGlyThrGlnThrCysGlyLeuIleGlnValThrLeuLeu | 1480 |
| Qy | 546  | GACACAGTGGAGCTGGCCACATACATGTGGCACCTTTCGACCTCCACAAAGAGTGGCTCC | 605  |
| Db | 1481 | AspThrValGluLeuAlaThrTyrThrValArgThrPheAlaLeuHisLysSerGlySer | 1500 |
| Qy | 606  | AGTGAGAGCGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT   | 665  |
| Db | 1501 | SerGluLysArgGluLeuArgGlnPheGlnPheMetAlaTrpProAspHisGlyValPro | 1520 |
| Qy | 666  | GAGTACCACACTCCATCTGGCCCTTCTTACGACGGGTCAAGGGCTGCAACCCCTAGAC   | 725  |

|    |      |   |      |
|----|------|---|------|
| Db | 1521 | GluTyrProThrProThrProThrProThrProThrProThrProThrProThrProThrPro | 1540 |
| Qy | 726  | GCAGGGCCCATGT     | 785  |
| Db | 1541 | AlaGlyProMetValValHisCysSerAlaGlyValGlyArgThrGlyCysPheIleVal    | 1560 |
| Qy | 786  | ATTGATCCCATGT     | 845  |
| Db | 1561 | IleAspAlaMetLeuGluArgMetLysHisGluLysThrValAspIleTyrGlyHisVal    | 1580 |
| Qy | 846  | ACCTGTCATGTCATCACAGAGAACTACATGTCGTGAGACGAGGACCACTGCTTTCATC      | 905  |
| Db | 1581 | ThrCysMetArgSerGlnArgAsnTyrMetValGlnThrGluAspGlnTyrValPheIle    | 1600 |
| Qy | 906  | CATGAGGCGT      | 965  |
| Db | 1601 | HisGluAlaLeuLeuGluAlaAlaThrCysGlyHisThrGluValProAlaArgAsnLeu    | 1620 |
| Qy | 966  | TATGCCCATCCAGAGCTGGGCGGAGTCCCTCCAGGGGAGAGTGTGACCGCATGGAG        | 1025 |
| Db | 1621 | TyrAlaHisIleGlnLysLeuGlyGlnValProProGlyGluSerValThrAlaMetGlu    | 1640 |
| Qy | 1026 | CTCGAGTTCAGT      | 1085 |
| Db | 1641 | LeuGluPheLysLeuLeuAlaSerSerLysAlaHisThrSerArgPheIleSerAlaAsn    | 1660 |
| Qy | 1086 | CTGCCCTGCAACAGTTCAGAACCCGCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT      | 1145 |
| Db | 1661 | LeuProCysAsnLysPheLysAsnArgLeuValAsnIleMetProTyrGluLeuThrArg    | 1680 |
| Qy | 1146 | GT        | 1205 |
| Db | 1681 | ValCysLeuGlnProIleArgGlyValGluGlySerAspTyrIleAsnAlaSerPheLeu    | 1700 |
| Qy | 1206 | GATGTTTATAGACAGCAGAGGCTTACATAGCTACACAGGGGCTCTGGCAGAGAGCACC      | 1265 |
| Db | 1701 | AspGlyTyrArgGlnGlnLysAlaTyrIleAlaThrGlnGlyProLeuAlaGluSerThr    | 1720 |
| Qy | 1266 | GAGGACTCTTGGCGCATGTCTATGGAGACAAATCCACCATCATCTGTCTGTGTGTGTGT     | 1325 |
| Db | 1721 | GluAspPheTrpArgMetLeuTrpGluHisAsnSerThrIleValMetLeuThrLys       | 1740 |
| Qy | 1326 | CTTGGGAGATGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG     | 1385 |
| Db | 1741 | LeuArgGluMetGlyArgGluLysCysHisGlnTyrTrpProAlaGluArgSerAlaArg    | 1760 |
| Qy | 1386 | TACCAGTACTTGT       | 1445 |
| Db | 1761 | TyrGlnTyrPheValValAspProMetAlaGluTyrAsnMetProGlnTyrIleLeuArg    | 1780 |
| Qy | 1446 | GAGTTCAGGTCTACGATGCCCCGGATGGGAGTGTGTGTGTGTGTGTGTGTGTGTGTGT      | 1505 |
| Db | 1781 | GluPheLysValThrAspAlaArgAspGlyGlnSerArgThrIleArgGlnPheGlnPhe    | 1800 |
| Qy | 1506 | ACAGACTGGCCACAGCAGGCGGCTGCCNAGACAGGCGGAGGATTCATTGATTCATCGG      | 1565 |
| Db | 1801 | ThrAspTrpProGluGlnGlyValProLysThrGlyGlyGlyPheIleAspPheIleGly    | 1820 |
| Qy | 1566 | CAGGTGTCATTAAGACCAAGGAGCAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT     | 1625 |
| Db | 1821 | GlnValHisLysThrLysGluGlnPheGlyGlnAspGlyProIleThrValHisCysSer    | 1840 |
| Qy | 1626 | GCTGGCGTGGCCGACCGGGGTGTTTCATCTGTGAGCATCTGTCTGTGGAGCGCATGCGC     | 1685 |
| Db | 1841 | AlaGlyValGlyArgThrGlyValPheIleThrLeuSerIleValLeuGluArgMetArg    | 1860 |
| Qy | 1686 | TATGAGGCGT        | 1745 |
| Db | 1861 | TyrGluGlyValValAspMetPheGlnThrValLysThrLeuArgThrGlnArgProAla    | 1880 |
| Qy | 1746 | ATCGTGCAGACAGCAGGACCATGATGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT      | 1805 |

Db 1881 MetValGlnThrGluAspGlnTyrGlnLeuCysTyrArgAlaAlaLeuGluTyrLeuGly 1900  
 QY 1806 AGCTTTGACCACTATGCAACG 1826  
 Db 1901 SerPheAspHisTyrAlaThr 1907

RESULT 3  
 US-09-925-300-950  
 ; Sequence 950, Application US/09925300  
 ; Patent No. US20020151681A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Craig Rosen,  
 ; APPLICANT: Steve Ruben  
 ; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies  
 ; FILE REFERENCE: PA101  
 ; CURRENT APPLICATION NUMBER: US/09/925,300  
 ; CURRENT FILING DATE: 2001-08-10  
 ; PRIOR APPLICATION NUMBER: PCT/US00/05988  
 ; PRIOR FILING DATE: 2000-03-08  
 ; PRIOR APPLICATION NUMBER: 60/124,270  
 ; PRIOR FILING DATE: 1999-03-12  
 ; NUMBER OF SEQ ID NOS: 1890  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 950  
 ; LENGTH: 442  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-09-925-300-950

Alignment Scores:  
 Pred. No.: 0 Length: 442  
 Score: 442.00 Matches: 442  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 38.84% Indels: 0  
 DB: 9 Gaps: 0

US-09-719-272-1 (1-3467) x US-09-925-300-950 (1-442)

QY 501 GCCCGTGGCAGCAGACCTGTGGCTTATTCAGGTCAACCTGTGTGACACAGTGGAGCTG 560  
 Db 1 AlaArgGlyThrGluThrCysGlyLeuIleGlnValThrLeuLeuAspThrValGluLeu 20  
 QY 561 GCCACATACATGTGGGACCTTGGCATTCCACCAAGAGTGGCTCCAGTGAGAGCGTGAG 620  
 Db 21 AlaThrTyrThrValArgThrPheAlaLeuHisLysSerGlySerGluLysArgGlu 40  
 QY 621 CTGGCTCAGTTTCAGTTCATGGCTGGCCAGACCATGGAGTTCCTCAGTACCACTCCC 680  
 Db 41 LeuArgGlnPheGlnPheMetAlaIrrProAspHisGlyValProGluTyrProThrPro 60  
 QY 681 ATCTCTGGCTTCTCTACGAGCGGTCAAGGCTGCAACCCCTAGACGAGGCGCCATGGTG 740  
 Db 61 IleLeuAlaPheLeuArgArgValLysAlaCysAsnProLeuAspAlaGlyProMetVal 80  
 QY 741 GTGCATCGACGCGGCGGTGGCCGCCACCGGCTGCTTCATCGTGAATTGATGCCATGTG 800  
 Db 81 ValHisCysSerAlaGlyValGlyArgThrGlyCysPheIleValIleAspAlaMetLeu 100  
 QY 801 GAGCGGATCAAGCAGCAGAGAGCGTGGACATCTATGGCCACCTGACCTGCGATCGCATCA 860  
 Db 101 GluArgMetLysHisGlyThrValAspIleTyrGlyHisValThrCysMetArgSer 120  
 QY 861 CAGAGGAACATACATGTGACAGCGGAGGACCACTAGCTGTTCATCATCAGGCGGTGCTG 920  
 Db 121 GlnArgAsnTyrMetValGlnThrGluAspGlnTyrValPheIleHisGluAlaLeuLeu 140  
 QY 921 GAGGCTGCCACGTGGCGGCACACAGAGTGCCTGCCCGCACTGATGCCACATCCAG 980  
 Db 141 GluAlaAlaThrCysGlyHisThrGluValProAlaArgAsnLeuTyrAlaHisIleGln 160  
 QY 981 AAGCTGGGCCAAGTGCCTCCAGGGGAGGTGTCACCGCATGGAGCTCGAGTTCAGATTG 1040

Db 161 LysLeuGlyGlnValProProGlyGluSerValThrAlaMetGluLeuGluPheLysLeu 180  
 QY 1041 CTGGCCAGCTCAAGGCCCCACACGTCCTCCGCTTTCATCAGCGCAACCTCCCTCCCAACAG 1100  
 Db 181 LeuAlaSerSerLysAlaHisThrSerArgPheIleSerAlaAsnLeuProCysAsnLys 200  
 QY 1101 TTCAGAACCGGCTGGTGAACATCATGCGCTACGAATTCACCCGTGTCTGCTGAGGCC 1160  
 Db 201 PheLysAsnArgLeuValAsnIleMetProTyrGluLeuThrArgValCysLeuGlnPro 220  
 QY 1161 ATCCGTGTGTGGAGGCTCTGACTACATCAATCAATCCAGCTCTCTGATGGTTATAGACAG 1220  
 Db 221 IleArgGlyValGluGlySerAspTyrIleAsnAlaSerPheLeuAspGlyTyrArgGln 240  
 QY 1221 CAGAAAGCCTACATAGCTACACAGGCGCTCTGGCAGAGAGCAGCAGAGACTTCTGGGCG 1280  
 Db 241 GlnLysAlaTyrIleAlaThrGlnGlyProLeuAlaGluSerThrGluAspPheTrpArg 260  
 QY 1281 ATGCTATGGAGGACCAATTCACCATCATCTGCTGCTGAGCAGCAGCTTCGGGAGATGGC 1340  
 Db 261 MetLeuTrpGluHisAsnSerThrIleIleValMetLeuThrLysLeuArgGluMetGly 280  
 QY 1341 AGGGAGAAATGCCACCACTACTGGCCAGCAGAGCGCTCTGCTCGCTACCACTTTGTT 1400  
 Db 281 ArgGluLysCysHisGlnTyrTrpProAlaGluArgSerAlaArgTyrGlnTyrPheVal 300  
 QY 1401 GTTGACCCGATGGCTGAGTACAAACATGCCCCAGTATATCTCGCTGAGTTCAGGTCCAG 1460  
 Db 301 ValAspProMetAlaGluTyrAsnMetProGlnTyrIleLeuArgGluPheLysValThr 320  
 QY 1461 GATGCCCGGATGGGCACTCAAGGACAATCCGGCAGTTCAGTTCACAGACTGGGCCAGAG 1520  
 Db 321 AspAlaArgAspGlyGlnSerArgThrIleArgGlnPheGlnPheThrAspTrpProGlu 340  
 QY 1521 CAGGGCGTGGCCACACAGAGGAGGATTCATTGACTTTCATCGGCGCAGGTGCATAGACC 1580  
 Db 341 GlnGlyValProLysThrGlyGluGlyPheIleAspPheIleGlnValHisLysThr 360  
 QY 1581 AAGGAGAGTTTGGACAGGATGGGCTTATCAGGTGCACTGCGTGGCTGGCGTGGCGCGC 1640  
 Db 361 LysGluGlnPheGlyGlnAspGlyProIleThrValHisCysSerAlaGlyValGlyArg 380  
 QY 1641 ACCGGGTGTTTCATCCTCAGCATCTGAGCATCTCTGGAGCGATCGCTATGAGGCGGTGGTC 1700  
 Db 381 ThrGlyValPheIleThrLeuSerIleValLeuGluArgMetArgTyrGluGlyValVal 400  
 QY 1701 GACATGTTTTCAGACCGTGAAGACCCCTGCGTACACAGCGTCTCTGCCATGGTCAGACAG 1760  
 Db 401 AspMetPheGlnThrValLysThrLeuArgThrGlnArgProAlaMetValGlnThrGlu 420  
 QY 1761 GACCATATCAGCTGTGCTACCGTGGCGGCTGGAGTACCTCGGAGCTTTCACCACTAT 1820  
 Db 421 AspGlnTyrGlnLeuCysTyrArgAlaAlaLeuGluTyrLeuGlySerPheAspHisTyr 440  
 QY 1821 GCAACG 1826  
 Db 441 AlaThr 442

RESULT 4  
 US-10-374-539-3  
 ; Sequence 3, Application US/10374539  
 ; Publication No. US20030195247A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: SUNESIS PHARMACEUTICALS, INC.  
 ; APPLICANT: BARR, Kenneth  
 ; APPLICANT: FAHR, Bruce  
 ; APPLICANT: HANSEN, Stig  
 ; APPLICANT: MCDOWELL, Robert  
 ; APPLICANT: WIESMAN, Chris  
 ; APPLICANT: ZHU, Jian  
 ; TITLE OF INVENTION: COMPOUNDS THAT MODULATE THE ACTIVITY OF  
 ; TITLE OF INVENTION: PTP-1B AND TC-PTP  
 ; FILE REFERENCE: 39750-0008

```

; CURRENT APPLICATION NUMBER: US/10/374,539
; CURRENT FILING DATE: 2003-02-25
; PRIOR APPLICATION NUMBER: US 60/361,475
; PRIOR FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 296
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-374-539-3

Alignment Scores:
Pred. No.: 6,388-260 Length: 296
Score: 296.00 Matches: 296
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 26.01% Indels: 0
DB: 14 Gaps: 0

US-09-719-272-1 (1-3467) x US-10-374-539-3 (1-296)
Qy 102 CCCATCACCAGCAGCTGCGGACCAACATCGAGCGCTTCAAGGCCAAGCTGCGCTCAAGTTC 161
Db 1 ProlleTherAspLeuAlaAsnValleAlaTyrAspHisSerArgVal 20
Qy 162 TCCGAGAGTATGAGTCCATCGACCTCGACAGCAGTTCACGTGGGAGAAATTCAAACCTG 221
Db 21 SerGlnGluTyrGluSerileAspProGlyGlnGlnPheThrTrpGluAsnSerAsnLeu 40
Qy 222 GAGGTGAACAGCCCAAGNACCGCTATCGGATGCTGATGCTAGCCTAGCACCCTCTCGAGTC 281
Db 41 GluValAsnLysProLysAsnArgTyrAlaAsnValleAlaTyrAspHisSerArgVal 60
Qy 282 ATCCTTACCTCTATCGATGGCTGCCCGGAGTGACTACATCAATGCCAATACATCGATCGAT 341
Db 61 IleLeuThrSerileAspGlyValProGlySerAspTyrIleAsnAlaAsnTyrIleAsp 80
Qy 342 GGCTACCGCAAGCAGATGCTTACATCGCCAGCAGGCGCCCTGCGGAGACCATGGC 401
Db 81 GlyTyrArgLysGlnAsnAlaTyrIleAlaThrGlnGlyProLeuProGluThrMetGly 100
Qy 402 GATTTCTGGAGATGGTGTGGGAACAGCGCCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 461
Db 101 AspPheTrpArgMetValTrpGlnGlnArgThrAlaThrValValMetMetThrArgLeu 120
Qy 462 GAGGAGAAGTCCCGGGTAAATGTGATCAGTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 521
Db 121 GluGluLysSerArgValLysCysAspGlnTyrTrpProAlaArgGlyThrGluThrCys 140
Qy 522 GGCTTTATTCAGTGACCTGTGGACACAGCGGACGCGCATGCTGCTGCTGCTGCTGCTGCTGCTG 581
Db 141 GlyLeuIleGlnValThrLeuLeuAspThrValGluLeuAlaThrTyrThrValArgThr 160
Qy 582 TTCGCATCTCCAAAGAGTGGCTCCAGTGAGAGAGCGTGAGCTGCTGCTGCTGCTGCTGCTGCTG 641
Db 161 PheAlaLeuHisLysSerGlySerSerGluLysArgGluLeuArgGlnPheGlnPheMet 180
Qy 642 GCTGCGCCAGACCATGAGTCTCTGAGTACCCCACTCCCTGCTGCTGCTGCTGCTGCTGCTGCTG 701
Db 181 AlaTrpProAspHisGlyValProGluTyrProThrProIleLeuAlaPheLeuArgArg 200
Qy 702 GTCAAGCGCTGCAACCCCTAGACGCGGCGCCATGGTGGTGCATCGCTGCTGCTGCTGCTGCTGCTG 761
Db 201 ValLysAlaCysAsnProLeuAspAlaGlyProMetValValHisCysSerAlaGlyVal 220
Qy 762 GCGCGCACCGCTGCTTCAATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 821
Db 221 GlyArgThrGlyCysPheIleValleAspAlaMetLeuGluArgMetLysHisGluLys 240
Qy 822 ACGGTGGACATCTATGCGCCAGCTGACCTGCATCGCATCACAGAGAACTACATGCTGTCAG 881
Db 241 ThrValAspIleGlyroGlyHisValThrCysMetArgSerGlnArgAsnTyrMetValGln 260

US-10-374-499-9
; Sequence 9, Application US/10374499
; Publication No. US20040005632A1
; GENERAL INFORMATION:
; APPLICANT: SUNESIS PHARMACEUTICALS, INC.
; APPLICANT: ERLANSON, Daniel A.
; APPLICANT: MCDOWELL, Robert S.
; TITLE OF INVENTION: METHODS FOR IDENTIFYING COMPOUNDS THAT
; TITLE OF INVENTION: MODULATE ENZYMAIC ACTIVITY
; FILE REFERENCE: 39750-0016
; CURRENT APPLICATION NUMBER: US/10/374,499
; CURRENT FILING DATE: 2003-02-25
; PRIOR APPLICATION NUMBER: US 60/377,034
; PRIOR FILING DATE: 2002-05-01
; PRIOR APPLICATION NUMBER: US 10/121,216
; PRIOR FILING DATE: 2002-04-10
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 296
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-374-499-9

Alignment Scores:
Pred. No.: 6,388-260 Length: 296
Score: 296.00 Matches: 296
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 26.01% Indels: 0
DB: 15 Gaps: 0

US-09-719-272-1 (1-3467) x US-10-374-499-9 (1-296)
Qy 102 CCCATCACCAGCAGCTGCGGACCAACATCGAGCGCTTCAAGGCCAAGCTGCGCTCAAGTTC 161
Db 1 ProlleTherAspLeuAlaAsnValleAlaTyrAspHisSerArgVal 20
Qy 162 TCCGAGAGTATGAGTCCATCGACCTCGACAGCAGTTCACGTGGGAGAAATTCAAACCTG 221
Db 21 SerGlnGluTyrGluSerileAspProGlyGlnGlnPheThrTrpGluAsnSerAsnLeu 40
Qy 222 GAGGTGAACAGCCCAAGNACCGCTATCGGATGCTGATGCTAGCCTAGCACCCTCTCGAGTC 281
Db 41 GluValAsnLysProLysAsnArgTyrAlaAsnValleAlaTyrAspHisSerArgVal 60
Qy 282 ATCCTTACCTCTATCGATGGCTGCCCGGAGTGACTACATCAATGCCAATACATCGATCGAT 341
Db 61 IleLeuThrSerileAspGlyValProGlySerAspTyrIleAsnAlaAsnTyrIleAsp 80
Qy 342 GGCTACCGCAAGCAGATGCTTACATCGCCAGCAGGCGCCCTGCGGAGACCATGGC 401
Db 81 GlyTyrArgLysGlnAsnAlaTyrIleAlaThrGlnGlyProLeuProGluThrMetGly 100
Qy 402 GATTTCTGGAGATGGTGTGGGAACAGCGCCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 461
Db 101 AspPheTrpArgMetValTrpGlnGlnArgThrAlaThrValValMetMetThrArgLeu 120
Qy 462 GAGGAGAAGTCCCGGGTAAATGTGATCAGTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 521
Db 121 GluGluLysSerArgValLysCysAspGlnTyrTrpProAlaArgGlyThrGluThrCys 140
Qy 522 GGCTTTATTCAGTGACCTGTGGACACAGCGGACGCGCATGCTGCTGCTGCTGCTGCTGCTGCTG 581
Db 141 GlyLeuIleGlnValThrLeuLeuAspThrValGluLeuAlaThrTyrThrValArgThr 160
Qy 582 TTCGCATCTCCAAAGAGTGGCTCCAGTGAGAGAGCGTGAGCTGCTGCTGCTGCTGCTGCTGCTG 641
Db 161 PheAlaLeuHisLysSerGlySerSerGluLysArgGluLeuArgGlnPheGlnPheMet 180
Qy 642 GCTGCGCCAGACCATGAGTCTCTGAGTACCCCACTCCCTGCTGCTGCTGCTGCTGCTGCTGCTG 701
Db 181 AlaTrpProAspHisGlyValProGluTyrProThrProIleLeuAlaPheLeuArgArg 200
Qy 702 GTCAAGCGCTGCAACCCCTAGACGCGGCGCCATGGTGGTGCATCGCTGCTGCTGCTGCTGCTGCTG 761
Db 201 ValLysAlaCysAsnProLeuAspAlaGlyProMetValValHisCysSerAlaGlyVal 220
Qy 762 GCGCGCACCGCTGCTTCAATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 821
Db 221 GlyArgThrGlyCysPheIleValleAspAlaMetLeuGluArgMetLysHisGluLys 240
Qy 822 ACGGTGGACATCTATGCGCCAGCTGACCTGCATCGCATCACAGAGAACTACATGCTGTCAG 881
Db 241 ThrValAspIleGlyroGlyHisValThrCysMetArgSerGlnArgAsnTyrMetValGln 260

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141 GlyLeuIleGlnValThrLeuLeuAspThrValGluLeuAlaThrTyrThrValArgThr 160  
582 TTGGCACTCCCAAGAGTGGCTCCAGTCAGAGCGTGCAGTTCAGTTTCATG 641  
161 PheAlaLeuHisLysSerGlySerGluLysArgGluLeuArgGlnPheMet 180  
642 GCCTGGCCAGACCACTGAGTTCCTGAGTACCACTCCCTCCCTGCTTCTTACGACGG 701  
181 AlaTrpProAspHisGlyValProGluTyrProThrProIleLeuAlaPheLeuArg 200  
702 GTCAGGCTGCAACCCCTAGACCCAGCGCCCATGTTGGTGTGCTGCTGAGCGCGCGT 761  
201 ValLysAlaCysAsnProLeuAspAlaGlyProMetValValHisCysSerAlaGlyVal 220  
762 GCGCGCACCGGCTGCTTCATCGTGTATGATGATGATGATGATGATGATGATGATGAT 821  
221 GlyArgThrGlyCysPheIleValIleAspAlaMetLeuGluArgMetLysHisGluLys 240  
822 ACGGTGACATCTATGGCCAGTGCATGCTGATGATGATGATGATGATGATGATGATGAT 881  
241 ThrValAspIleTyrGlyHisValThrCysMetArgSerGlnArgAsnTyrMetValGln 260  
882 ACGGAGGACCACTGCTGCTTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 941  
261 ThrGluAspGlnTyrValPheIleHisGluAlaLeuLeuGluAlaAlaThrCysGlyHis 280  
942 ACAGAGGTGCTGCGCGCAACCTGTATGCCACATCCAGAGCTGGC 989  
281 ThrGluValProAlaArgAsnLeuTyrAlaHisIleGlnLysLeuGly 296

## RESULT 6

US-10-314-232-13  
; Sequence 13, Application US/10314232  
; Publication No. US20030138932A1  
; GENERAL INFORMATION:  
; APPLICANT: MOLLER, NIELS P.H.  
; APPLICANT: MOLLER, KARIN B.  
; APPLICANT: ULLRICH, AXEL  
; TITLE OF INVENTION: PTP-S31: A NOVEL PROTEIN TYROSINE PHOSPHATASE  
; FILE REFERENCE: 038602/0686  
; CURRENT APPLICATION NUMBER: US/10/314,232  
; PRIOR FILING DATE: 2002-12-09  
; PRIOR APPLICATION NUMBER: US/09/361,096  
; PRIOR FILING DATE: 1999-07-26  
; PRIOR APPLICATION NUMBER: 08/449,609  
; PRIOR FILING DATE: 1995-05-24  
; PRIOR APPLICATION NUMBER: 08/036,210  
; PRIOR FILING DATE: 1995-03-23  
; NUMBER OF SEQ ID NOS: 53  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 13  
; LENGTH: 289  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: LAR  
US-10-314-232-13

Alignment Scores:  
Pred. No.: 1.5e-253 Length: 289  
Score: 289.00 Matches: 289  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 25.40% Indels: 0  
DB: 14 Gaps: 0

US-09-719-272-1 (1-3467) x US-10-314-232-13 (1-289)

QY 81 ATGCGAGACCAACCCATCCCATCCAGCTGGCGGACCAACATCGAGCGCTCAAA 140  
DB 1 MetArgAspHisProProlleProIleThrAspLeuAlaAspAsnIleGluArgLeuLys 20

QY 141 GCCAACGATGGCTCAAGTTCTCCAGAGTATGAGTCCATCGACCTCGACACGACGCTTC 200  
DB 21 AlaAsnAspGlyLeuLysPheSerGlnGluTyrGluSerIleAspProGlyGlnGlnPhe 40  
QY 201 ACGTGGGAGAAATTCAAACCTCGAGGTCAACAAAGCCCAAGAACCCCTATGCGAAATGTCTATC 260  
DB 41 ThrTrpGluAsnSerAsnLeuGluValAsnLysProlLysAsnArgTyrAlaAsnValIle 60  
QY 261 GCCTACACCACTCTCGAGTCATCTTACCTCTATCATGCGCTCCCGGAGTGACTAC 320  
DB 61 AlaTyrAspHisSerArgValIleLeuThrSerIleAspGlyValProGlySerAspTyr 80  
QY 321 ATCAATCCCACTACATGATGGCTACCGCAAGCAGAAATGCCTACATCGCCACGACGCGC 380  
DB 81 IleAsnAlaAsnTyrIleAspGlyTyrArgLysGlnAsnAlaTyrIleAlaThrGlnGly 100  
QY 381 CCCCTGCCAGACCATGGCGCATTTCTGGAGAAATGGTGGGAAACAGCGCACGCCCACT 440  
DB 101 ProlLeuProGluThrMetGlyAspPheTrpArgMetValTrpGluGlnArgThrAlaThr 120  
QY 441 GTGTCATGATGACACCGCTGGAGGAGAGTCCCGGGTAAATGTGATCAGTACTGCGCA 500  
DB 121 ValValMetMetThrArgLeuGluLysSerArgValLysCysAspGlnTyrTrpPro 140  
QY 501 GCCCGTGGCACCGAGACTGTGGCTTATTCAGGTGACCTGTTGGACACAGTGGAGCTG 560  
DB 141 AlaArgGlyThrGluThrCysGlyLeuIleGlnValThrLeuLeuAspThrValGluLeu 160  
QY 561 GCCACATACACTGTGCGCACCTTCGCACCTCCACAAAGAGTGGCTCCAGTGAGAGCGTGAG 620  
DB 161 AlaThrTyrThrValArgThrPheAlaLeuHisLysSerGlySerSerGluLysArgGlu 180  
QY 621 CTGCTCAGTTTCAGTTCATGGCTGGCCAGACCATGAGTTCCTGAGTACCCAACTCCC 680  
DB 181 LeuArgGlnPheGlnPheMetAlaTrpProAspHisGlyValProGluTyrProThrPro 200  
QY 681 ATCTGGCTTCCTACGACGGTCAAGCTGCAACCCCTAGACGAGGCGGCGCCATGGT 740  
DB 201 IleLeuAlaPheLeuArgValLysAlaCysAsnProLeuAspAlaGlyProMetVal 220  
QY 741 GTGCACTGCGAGCGGGCGTGGCGCGCACCGGCTGCTTCATCGTGTGATGATGATGATGAT 800  
DB 221 ValHisCysSerAlaGlyValGlyArgThrGlyCysPheIleValIleAspAlaMetLeu 240  
QY 801 GAGCGGATGAAGACGAGAGACCGGTGACATCTATGCGCACGCTGACCTGATGCGATCA 860  
DB 241 GluArgMetLysHisGluLysThrValAspIleTyrGlyHisValThrCysMetArgSer 260  
QY 861 CAGAGGAACTACATGTTGCGACGCGGAGGACAGTACGTTGTTCCATCCATGAGCGCTGCTG 920  
DB 261 GlnArgAsnTyrMetValGlnThrGluAspGlnTyrValPheIleHisGluAlaLeuLeu 280  
QY 921 GAGCTGCCACGTGGCGCCACACAGAG 947  
DB 281 GluAlaAlaThrCysGlyHisThrGlu 289

## RESULT 7

US-09-788-626-8  
; Sequence 8, Application US/09788626  
; Patent No. US20020009762A1  
; GENERAL INFORMATION:  
; APPLICANT: Flint, Andrew J.  
; APPLICANT: Cool, Deborah E.  
; TITLE OF INVENTION: IMPROVED ASSAY FOR PROTEIN TYROSINE  
; TITLE OF INVENTION: PHOSPHATES  
; FILE REFERENCE: 200125,401  
; CURRENT APPLICATION NUMBER: US/09/788,626  
; CURRENT FILING DATE: 2001-02-13  
; NUMBER OF SEQ ID NOS: 40  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 8  
; LENGTH: 306  
; TYPE: PRT

ORGANISM: Homo sapiens  
US-09-788-626-8

## Alignment Scores:

Pred. No.: 2,116-174 Length: 306  
Score: 202.00 Matches: 250  
Percent Similarity: 97.66% Conservative: 0  
Best Local Similarity: 97.66% Mismatches: 6  
Query Match: 17.75% Indels: 6  
DB: 9 Gaps: 0

US-09-719-272-1 (1-3467) x US-09-788-626-8 (1-306)

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QY 195 CAGTTCAGTGGAGAGATTCAACCTGGAGTGAACAGCCCAAGAACCGCTATGCAAT 254
Db 1 GlnPheThrTrpGluAsnSerAsnLeuGluValAsnLysProLysAsnArgTyrAlaAsn 20
QY 255 GTCATCGCTTACGACCACTCTCGAGTCATCTTACCTCTATCATGCGCGTCCCGGAGT 314
Db 21 ValIleAlaTyrAspHisSerArgValIleLeuThrSerIleAspGlyValProGlySer 40
QY 315 GACTACATCAATCCCACTACATCGATGGCTACCGAAGCAGAAATGCTTACATCGCCACG 374
Db 41 AspTyrIleAsnAlaAsnTyrIleAspGlyTyrArgLysGlnAsnAlaTyrIleAlaThr 60
QY 375 CAGGGCCCTGCGCAGACCATCGGCGATTTCTGGAGATGCTGTGGNAACAGCGCAG 434
Db 61 GlnGlyProLeuProGluThrMetGlyAspPheTrpArgMetValTrpGluGlnArgThr 80
QY 435 GCCACTGTGTGTCATGATGACACCGCTGGAGGAGAAGTCCCGGTAATAATGTGATCAGTAC 494
Db 81 AlaThrValValMetMetThrArgLeuGluGluLysSerArgValLysCysAspGlnTyr 100
QY 495 TGCCACGCCCGTGGCCAGACCTGTGGCTTATTACAGTGACCTGTGGACACAGTG 554
Db 101 TrpProAlaArgGlyThrGluThrCysGlyLeuIleGlnValThrLeuLeuAspThrVal 120
QY 555 GAGCTGGCCACATACACTGTGGCCACTTCGCCTCCCAAGAGTGGCTCCAGTGAGAAG 614
Db 121 GluLeuAlaThrTyrThrVal-----PheAlaLeuHisLysSerGlySerGluLys 138
QY 615 CGTGAGCTGCTGAGTTTCAGTTTCATGCGCTGCGCCAGACCATGGAGTTCCTGAGTACCCA 674
Db 139 ArgGluLeuArgGlnPheGlnPheMetAlaTrpProAspHisGlyValProGluTyrPro 158
QY 675 ATCCCATCTGCTGCTTCTTACGACCGGTTCAAGCTTGCAACCCCTAGACGCGGCCC 734
Db 159 ThrProIleLeuAlaPheLeuArgValLysAlaCysAsnProLeuAspAlaGlyPro 178
QY 735 ATGGTGTGCACTGACGCGCGGCGTGGCGCGCACCGGCTGCTTCATCGTATTGATGCC 794
Db 179 MetValValHisCysSerAlaGlyValGlyArgThrGlyCysPheIleValIleAspAla 198
QY 795 ATGTTGGAGCGGATGAAGCACGAGAACGCTGGACATCTATGGCCACGCTGACCTGCATG 854
Db 199 MetLeuGluArgMetLysHisGlyLysThrValAspIleTyrGlyHisValThrCysMet 218
QY 855 CGATCAGAGGAACTACATGTTGTCAGACGAGGAGCAGTACGTGTTTCATCCATGAGGG 914
Db 219 ArgSerGlnArgAsnTyrMetValGlnThrGluAspGlnTyrValPheIleHisGluAla 238
QY 915 CTGCTGGAGGCTCCGACGCTGGCGCCACACAGAGGTG 950
Db 239 LeuLeuGluAlaAlaThrCysGlyHisThrGluVal 250
```

## RESULT 8

US-09-788-626-27  
Sequence 27, Application US/09788626  
Patent No. US2002009762A1  
GENERAL INFORMATION:  
APPLICANT: Flint, Andrew J.  
APPLICANT: Cool, Deborah E.  
TITLE OF INVENTION: IMPROVED ASSAY FOR PROTEIN TYROSINE

## TITLE OF INVENTION: PHOSPHATES

FILE REFERENCE: 200125.401  
CURRENT APPLICATION NUMBER: US/09/788,626  
CURRENT FILING DATE: 2001-02-13  
NUMBER OF SEQ ID NOS: 40  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 27  
LENGTH: 294  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-788-626-27

## Alignment Scores:

Pred. No.: 7,5e-170 Length: 294  
Score: 197.00 Matches: 245  
Percent Similarity: 97.61% Conservative: 0  
Best Local Similarity: 97.61% Mismatches: 6  
Query Match: 17.31% Indels: 6  
DB: 9 Gaps: 0

US-09-719-272-1 (1-3467) x US-09-788-626-27 (1-294)

```
QY 1062 ACGTCCCGCTTCATCAGCGCCCAACCTGCCCTGCCAACAAAGTTCAAGAACCGGTGTGAAC 1121
Db 1 ThrSerArgPheIleSerAlaAsnLeuProCysAsnLysPheLysAsnArgLeuValAsn 20
QY 1122 ATCATGCCCTACGAATTGACCCGCTGTGTCTGTCTGCGAGCCCATCCGTGCTGTGAGGCTCT 1181
Db 21 IleMetProTyrGluLeuThrArgValCysLeuGlnProIleArgGlyValGluGlySer 40
QY 1182 GACTACATCAATGCCAGCTTCTCTGGATGTTATAGACAGACAGAGCCCTACATAGTACA 1241
Db 41 AspTyrIleAsnAlaSerPheLeuAspGlyTyrArgGlnGlnLysAlaTyrIleAlaThr 60
QY 1242 CAGGGCGCTCTGCGCAGAGACACCGAGGACTTCTGCGCATCTATGGAGACACAATTC 1301
Db 61 GlnGlyProLeuAlaGluSerThrGluAspPheTrpArgMetLeuTrpGluHisAsnSer 80
QY 1302 ACATCATCTCATCTGTCGACCAAGCTTCGGAGATGGCGAGGAGAAATGCCACAGTAC 1361
Db 81 ThrIleValMetLeuThrLysLeuArgGluMetGlyArgGlyLysCysHisGlnTyr 100
QY 1362 TGGCCAGCAGAGCGCTCTGCTCGCTACCAAGTACTTGTGTGTGACCCGATGGCTGAGTAC 1421
Db 101 TrpProAlaGluArgSerAlaArgTyrGlnTyrPheValValAspProMetAlaGluTyr 120
QY 1422 AACATGCCCGCTATATCTGCTGAGTTCAAAGTCAAGTCCCGGATCGGCAGTCA 1481
Db 121 AsnMetProGlnTyrIleLeu-----PheLysValThrAspAlaAspGlyGlnSer 138
QY 1482 AGACAAATCCGCGAGTTCAGTTTCAGACTGCGCCAGAGCAGGCGTGCACAGCAGC 1541
Db 139 ArgThrIleArgGlnPheGlnPheThrAspTrpProGluGlnGlyValProLysThrGly 158
QY 1542 GAGGATTCATTGACTTTCATCCGGCAGGTGCATAAGACCAAGCAGCAGTTCGACAGGAT 1601
Db 159 GluGlyPheIleAspPheIleGlyGlnValHisLysThrLysGluGlnPheGlyGlnAsp 178
QY 1602 GGGCTTATCAGCGTCACGTGCTGCGTGGCGCCGACCCGGGTGTTCATCACTCTG 1661
Db 179 GlyProIleThrValHisCysSerAlaGlyValGlyArgThrGlyValPheIleThrLeu 198
QY 1662 AGCATCGCTCTGGAGCGCATGCGCTATGAGGCGGTGGTGCACATGTTTCAGACCGGTGAG 1721
Db 199 SerIleValLeuGluArgMetArgTyrGluGlyValValAspMetPheGlnThrValLys 218
QY 1722 ACCCTGCGTACACAGCGTCTCTGCCATGGTGCAGACAGAGGACAGTATCAGTGTGCTAC 1781
Db 219 ThrLeuArgThrGlnArgProAlaMetValGlnThrGluAspGlnTyrGlnLeuCysTyr 238
QY 1782 CGTGGCGCTCGAGTACCTC 1802
Db 239 ArgAlaAlaLeuGluTyrLeu 245
```

```
RESULT 9
US-09-808-602-54
; Sequence 54, Application US/09808602
; Patent No. US20020155115A1
; GENERAL INFORMATION:
; APPLICANT: Vernet, Corine A
; APPLICANT: Fernandes, Elma
; APPLICANT: Shimkets, Richard A
; APPLICANT: Herrman, John L
; APPLICANT: Majumder, Kumud
; APPLICANT: Mishra, Vishnu
; APPLICANT: Mezes, Peter S
; APPLICANT: MacDougall, John
; TITLE OF INVENTION: NO. US20020155115A1el Proteins and Nuclec Acids Encoding Same
; FILE REFERENCE: 15966-697 CIP
; CURRENT APPLICATION NUMBER: US/09/808,602
; CURRENT FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: 09/800,198
; PRIOR FILING DATE: 2001-03-05
; PRIOR APPLICATION NUMBER: 60/186,596
; PRIOR FILING DATE: 2000-03-03
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 54
; LENGTH: 1502
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-808-602-54

Alignment Scores:
Pred. No.: 2.14e-44 Length: 1502
Score: 59.00 Matches: 59
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 5.18% Indels: 0
DB: 9 Gaps: 0

US-09-719-272-1 (1-3467) x US-09-808-602-54 (1-1502)
QY 1311 GTCATGCTGACCAAGCTTCGGGAGATGGCGAGAGAAATGCCACGAGTACTGGCCAGCA 1370
DB 1331 ValMetLeuThrLysLeuArgGluMetGlyArgGluLysCysHisGlnTyrTrpProAla 1350
QY 1371 GAGCGCTCTGCTCGCTACCAAGTACTTTGTTGTGACCCGATGGCTGAGTACAAATGCC 1430
DB 1351 GluArgSerAlaArgTyrGlnTyrPheValValAspProMetAlaGluTyrAsnMetPro 1370
QY 1431 CAGTATATCTCGTGCAGTTCAGGTCAAGTCACGGATGCCGGGATGGCGAGTCAAGGACA 1487
DB 1371 GlnTyrIleuArgGluPheLysValThrAspAlaArgAspGlyGlnSerArgThr 1389

RESULT 10
US-09-808-198-44
; Sequence 44, Application US/09800198
; Publication No. US20030087816A1
; GENERAL INFORMATION:
; APPLICANT: Vernet, Corine AM
; APPLICANT: Fernandes, Elma
; APPLICANT: Shimkets, Richard A
; APPLICANT: Herrmann, John L
; APPLICANT: Majumder, Kumud
; APPLICANT: Mishra, Vishna
; APPLICANT: Mezes, Peter S
; APPLICANT: Rastelli, Luca
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 15966-697
; CURRENT APPLICATION NUMBER: US/09/800,198
; CURRENT FILING DATE: 2001-03-05
; PRIOR APPLICATION NUMBER: 60/186,596
; PRIOR FILING DATE: 2000-03-03
; NUMBER OF SEQ ID NOS: 98
; SOFTWARE: Patentin Ver. 2.1
US-09-719-272-1 (1-3467) x US-09-808-602-54 (1-1502)
QY 1311 GTCATGCTGACCAAGCTTCGGGAGATGGCGAGAGAAATGCCACGAGTACTGGCCAGCA 1370
DB 1331 ValMetLeuThrLysLeuArgGluMetGlyArgGluLysCysHisGlnTyrTrpProAla 1350
QY 1371 GAGCGCTCTGCTCGCTACCAAGTACTTTGTTGTGACCCGATGGCTGAGTACAAATGCC 1430
DB 1351 GluArgSerAlaArgTyrGlnTyrPheValValAspProMetAlaGluTyrAsnMetPro 1370
QY 1431 CAGTATATCTCGTGCAGTTCAGGTCAAGTCACGGATGCCGGGATGGCGAGTCAAGGACA 1487
DB 1371 GlnTyrIleuArgGluPheLysValThrAspAlaArgAspGlyGlnSerArgThr 1389

RESULT 11
US-09-808-602-55
; Sequence 55, Application US/09808602
; Patent No. US20020155115A1
; GENERAL INFORMATION:
; APPLICANT: Vernet, Corine A
; APPLICANT: Fernandes, Elma
; APPLICANT: Shimkets, Richard A
; APPLICANT: Herrman, John L
; APPLICANT: Majumder, Kumud
; APPLICANT: Mishra, Vishnu
; APPLICANT: Mezes, Peter S
; APPLICANT: MacDougall, John
; TITLE OF INVENTION: NO. US20020155115A1el Proteins and Nuclec Acids Encoding Same
; FILE REFERENCE: 15966-697 CIP
; CURRENT APPLICATION NUMBER: US/09/808,602
; CURRENT FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: 09/800,198
; PRIOR FILING DATE: 2001-03-05
; PRIOR APPLICATION NUMBER: 60/186,596
; PRIOR FILING DATE: 2000-03-03
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 55
; LENGTH: 1948
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-808-602-55

Alignment Scores:
Pred. No.: 2.07e-44 Length: 1948
Score: 59.00 Matches: 59
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 5.18% Indels: 0
DB: 9 Gaps: 0

US-09-719-272-1 (1-3467) x US-09-808-602-55 (1-1948)
QY 1311 GTCATGCTGACCAAGCTTCGGGAGATGGCGAGAGAAATGCCACGAGTACTGGCCAGCA 1370
DB 1777 ValMetLeuThrLysLeuArgGluMetGlyArgGluLysCysHisGlnTyrTrpProAla 1796
QY 1371 GAGCGCTCTGCTCGCTACCAAGTACTTTGTTGTGACCCGATGGCTGAGTACAAATGCC 1430
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; SEQ ID NO 44
; LENGTH: 1502
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-800-198-44

Alignment Scores:
Pred. No.: 2.14e-44 Length: 1502
Score: 59.00 Matches: 59
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 5.18% Indels: 0
DB: 10 Gaps: 0
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US-09-719-272-1 (1-3467) x US-09-800-198-44 (1-1502)
QY 1311 GTCATGCTGACCAAGCTTCGGGAGATGGCGAGAGAAATGCCACGAGTACTGGCCAGCA 1370
DB 1331 ValMetLeuThrLysLeuArgGluMetGlyArgGluLysCysHisGlnTyrTrpProAla 1350
QY 1371 GAGCGCTCTGCTCGCTACCAAGTACTTTGTTGTGACCCGATGGCTGAGTACAAATGCC 1430
DB 1351 GluArgSerAlaArgTyrGlnTyrPheValValAspProMetAlaGluTyrAsnMetPro 1370
QY 1431 CAGTATATCTCGTGCAGTTCAGGTCAAGTCACGGATGCCGGGATGGCGAGTCAAGGACA 1487
DB 1371 GlnTyrIleuArgGluPheLysValThrAspAlaArgAspGlyGlnSerArgThr 1389
```

```
RESULT 11
US-09-808-602-55
; Sequence 55, Application US/09808602
; Patent No. US20020155115A1
; GENERAL INFORMATION:
; APPLICANT: Vernet, Corine A
; APPLICANT: Fernandes, Elma
; APPLICANT: Shimkets, Richard A
; APPLICANT: Herrman, John L
; APPLICANT: Majumder, Kumud
; APPLICANT: Mishra, Vishnu
; APPLICANT: Mezes, Peter S
; APPLICANT: MacDougall, John
; TITLE OF INVENTION: NO. US20020155115A1el Proteins and Nuclec Acids Encoding Same
; FILE REFERENCE: 15966-697 CIP
; CURRENT APPLICATION NUMBER: US/09/808,602
; CURRENT FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: 09/800,198
; PRIOR FILING DATE: 2001-03-05
; PRIOR APPLICATION NUMBER: 60/186,596
; PRIOR FILING DATE: 2000-03-03
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 55
; LENGTH: 1948
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-808-602-55
```

```
Alignment Scores:
Pred. No.: 2.07e-44 Length: 1948
Score: 59.00 Matches: 59
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 5.18% Indels: 0
DB: 9 Gaps: 0
```

```
US-09-719-272-1 (1-3467) x US-09-808-602-55 (1-1948)
QY 1311 GTCATGCTGACCAAGCTTCGGGAGATGGCGAGAGAAATGCCACGAGTACTGGCCAGCA 1370
DB 1777 ValMetLeuThrLysLeuArgGluMetGlyArgGluLysCysHisGlnTyrTrpProAla 1796
QY 1371 GAGCGCTCTGCTCGCTACCAAGTACTTTGTTGTGACCCGATGGCTGAGTACAAATGCC 1430
```



```
Db 1797 GluArgSerAlaArgTyrGlnTyrPheValValAspProMetAlaGluTyrAsnMetPro 1816
Qy 1431 CAGTATATCTGCGTGTAGTTCAAGGTCAAGGATCCCGGAGTGGCGAGTCAAGGACA 1487
Db 1817 GlnTyrIleLeuArgGluPheLysValThrAspAlaArgAepGlyGlnSerArgThr 1835

RESULT 12
US-09-800-198-45
; Sequence 45, Application US/09800198
; Publication No. US20030087816A1
; GENERAL INFORMATION:
; APPLICANT: Vernet, Cornie AM
; APPLICANT: Fernandes, Elma
; APPLICANT: Shimkets, Richard A
; APPLICANT: Herrmann, John L
; APPLICANT: Majumder, Kumud
; APPLICANT: Mishra, Vishna
; APPLICANT: Mezes, Peter S
; APPLICANT: Rastelli, Luca
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 15966-697
; CURRENT APPLICATION NUMBER: US/09/800,198
; CURRENT FILING DATE: 2001-03-05
; PRIOR APPLICATION NUMBER: 60/186,596
; PRIOR FILING DATE: 2000-03-03
; NUMBER OF SEQ ID NOS: 98
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 45
; LENGTH: 1948
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-800-198-45

Alignment Scores:
Pred. No.: 2,07e-44 Length: 1948
Score: 59.00 Matches: 59
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 5.18% Indels: 0
DB: Gaps: 0

US-09-719-272-1 (1-3467) x US-09-800-198-45 (1-1948)

Qy 1311 GTCATGTGTACCAAGCTTCGGAGATGGCAGGAGAAATGCCACAGTACTGCCAGCA 1370
Db 1777 ValMetLeuThrLysLeuArgGluMetGlyArgGluLysCysHisGlnTyrTrpProAla 1796
Qy 1371 GAGCGCTCTGCTGCTACCAAGTACTTTGTTGTTGACCCGATGGCTGAGTACCAATGCC 1430
Db 1797 GluArgSerAlaArgTyrGlnTyrPheValValAspProMetAlaGluTyrAsnMetPro 1816
Qy 1431 CAGTATATCTGCGTGTAGTTCAAGGTCAAGGATCCCGGAGTGGCGAGTCAAGGACA 1487
Db 1817 GlnTyrIleLeuArgGluPheLysValThrAspAlaArgAepGlyGlnSerArgThr 1835

RESULT 13
US-10-029-386-29636
; Sequence 29636, Application US/10029386
; Publication No. US20030194704A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR G
; FILE REFERENCE: AEOMICA-X-2
; CURRENT APPLICATION NUMBER: US/10/029,386
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 34288
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 29636
; LENGTH: 57
; TYPE: PRT
```

```
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC011772.3
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.9
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.4
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 8.5
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.4
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.4
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.2
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.95
; OTHER INFORMATION: SWISSPROT HIT: O00470, EVALUE 1.20e+00
US-10-029-386-29636

Alignment Scores:
Pred. No.: 1,46e-40 Length: 57
Score: 55.00 Matches: 55
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 4.86% Indels: 0
DB: Gaps: 0

US-09-719-272-1 (1-3467) x US-10-029-386-29636 (1-57)

Qy 476 CCGGAGACTTCTCTCCAGCGGTGTCTCATCATGACACAGTGGCGCTGCTGTTCCACAC 417
Db 3 ProGlyLeuLeuLeuGlnProCysHisHisAspHisSerGlyArgAlaLeuPheProHis 22
Qy 416 CATTCTCCAGAAATCCCCATGCTCTCGGCGAGGGGGCCCTCGTGGCGAGTAGGCAATT 357
Db 23 HisSerProGluIleAlaHisGlyLeuGlyGlnGlyAlaLeuArgGlyAepValGlyIle 42
Qy 356 CTGCTTGGCGTAGCCATCGATGCTAGTGGCATGTAGTCACT 312
Db 43 LeuLeuAlaValAlaIleAepValValGlyIleAepValValThr 57

RESULT 14
US-10-258-666-12
; Sequence 12, Application US/10258666
; Publication No. US20040005578A1
; GENERAL INFORMATION:
; APPLICANT: Yamada, Yoji
; APPLICANT: Sekine, Susumu
; APPLICANT: Kikuchi, Yasuhiro
; APPLICANT: Sakurada, Kazuhiro
; APPLICANT: Kyowa Hakko Kogyo Co., Ltd.
; TITLE OF INVENTION: Myocardial Cell Proliferation-Associated Genes
; FILE REFERENCE: 082382-000000US
; CURRENT APPLICATION NUMBER: US/10/258,666
; CURRENT FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: JP 2000-126741
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: WO PCT/JP01/03700
; PRIOR FILING DATE: 2001-04-27
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 1495
; TYPE: PRT
; ORGANISM: Rattus norvegicus
; FEATURE:
; OTHER INFORMATION: RHDH-231, PTP-P1
US-10-258-666-12

Alignment Scores:
Pred. No.: 4,14e-27 Length: 1495
Score: 40.00 Matches: 40
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.51% Indels: 0
DB: Gaps: 0

US-09-719-272-1 (1-3467) x US-10-258-666-12 (1-1495)
```

|    |      |   |                           |                                   |      |
|----|------|---|---------------------------|-----------------------------------|------|
| Qy | 1311 | GTCA  | TGCTGACCAAGCTTCGGGAGATGGG | CAGGAGAGAAATGCCACCAAGTACTGGCCAGCA | 1370 |
| Db | 1327 | ValMetLeuThr  | LySLeuArgGluMetGlyArgGlu  | ylsCysHisGlnTyrTrpProAla          | 1346 |
| Qy | 1371 | GAGCGCTCTGCTCGCTACCAAGTACTTGTGTGTGTGACCCGATGGCTGAGTACAACATGCCCC |                           |                                   | 1430 |
| Db | 1347 | GluArgSerAlaArgTyrGlnTyrPheValValAspProMetAlaGlnTyrAsnMetPro    |                           |                                   | 1366 |

Db  
RESUM.T 15

```

US-10-087-684-38
; Sequence 38, Application US/10087684
; Publication No. US20040029116A1
; GENERAL INFORMATION:
; APPLICANT: Edinger, Shlomit R.
; APPLICANT: MacDougall, John R.
; APPLICANT: Millet, Isabelle
; APPLICANT: Ellerman, Karen
; APPLICANT: Stone, David J.
; APPLICANT: Grosse, William M.
; APPLICANT: Lepley, Denise M.
; APPLICANT: Rieser, Daniel K.
; APPLICANT: Burgess, Catherine E.
; APPLICANT: Casman, Stacie, J.
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Boldog, Ferenc L.
; APPLICANT: Li, Li
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Mishra, Vishnu
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Rastelli, Luca
; APPLICANT: Tchernev, Velizar T.
; APPLICANT: Vernet, Corine A.M.
; APPLICANT: Zethusen, Bryan D.
; APPLICANT: Malyankar, Uriel M.
; APPLICANT: Guo, Xiaojia
; APPLICANT: Miller, Charles E.
; APPLICANT: Gangolli, Esha A.
; TITLE OF INVENTION: PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 21402-214 CIP
; CURRENT APPLICATION NUMBER: US/10/087,684
; CURRENT FILING DATE: 2003-03-10
; PRIOR APPLICATION NUMBER: 60/253,834
; PRIOR FILING DATE: 2000-11-29
; PRIOR APPLICATION NUMBER: 60/250,926
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: 60/264,180
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 60/274,194
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: 60/313,656
; PRIOR FILING DATE: 2001-08-20
; PRIOR APPLICATION NUMBER: 60/327,456
; PRIOR FILING DATE: 2001-10-05
; NUMBER OF SEQ ID NOS: 220
; SOFTWARE: CuraseqList version 0.1
; SEQ ID NO 38
; LENGTH: 2029
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-10-087-684-38

```

| Alignment Scores:      |          |               |
|------------------------|----------|---------------|
| Pred. No.:             | 1.14e-21 | Length:       |
| Score:                 | 34.00    | Matches:      |
| Percent Similarity:    | 100.00%  | Conservative: |
| Best Local Similarity: | 100.00%  | Mismatches:   |
| Query Match:           | 2.99%    | Indels:       |
| DB:                    | 12       | Gaps:         |
|                        |          | 2029          |

US-09-719-272-1 (1-3467) x US-10-087-684-38 (1-2029)

Qy 1539 GGCAGGGATTCAATTGACTTCATCGGGCAGGTGCATAAGACCAAGGACGAGTTTGGACAG 1598